

**IN THE SPECIFICATION**

The current amendment is made with relation to the original specification filed 31<sup>st</sup> October 2003 which is understood to be the specification of record.

Please replace current paragraph [0022] with the following paragraph:

**[0022] b) Identification of candidate genes from associations of measured clinical factors (e.g., cholesterol levels) that correlate with disease:** Cholesterol levels that are 1.2X the recommended level of 200 mg/dl have a 2 fold greater risk of heart disease (~~American Heart Association:~~  
(~~<http://www.americanheart.org/presenter.jhtml?identifier=4500>~~). Researchers therefore targeted the control point of the cholesterol biosynthetic pathway for development of drugs (statins) to control the level of total serum cholesterol. Statins do reduce cholesterol levels and reduce the *relative risk* of coronary heart disease by ~25%. However, the absolute reduction in risk in one study (as an example) was 8.3 percent in the placebo group to 6.4% in the pravastatin treated group ([13] other references are in ACC/AHA/NHLBI Clinical Advisory on the Use and Safety of Statins, ~~found at:~~  
~~<http://www.nhlbi.nih.gov/guidelines/cholesterol/statins.htm>~~).

Please replace current paragraph [0029] with the following paragraph:

**[0029] d) Identification of chromosomal regions associated with disease and chose most likely candidate genes within those regions:** Genetic methods called quantitative trait loci (QTL) analyses have been developed over the past 15 years that identify regions of chromosomes encoding one or more genes that contribute to the development of complex disease [14-16]. Insulin-dependent diabetes mellitus (IDDM) is an example of the power and limitations of this approach. There are about 15 QTL loci, (IDDM1 through NIDDM15) regulating insulin, glucose, lipid, or hormone levels that directly contribute to diabetes development.

Approximately 500 QTLs for diabetes, obesity, cancer, and other conditions have been determined in laboratory animals

([http://www.informatics.jax.org/searches/marker\\_report.cgi](http://www.informatics.jax.org/searches/marker_report.cgi)) and a smaller subset in humans.